

SEQUENCE LISTING

<110> Li, Lhing-Yew  
Trei, Kelli J.

<120> Polynucleotide Constructs for Increased Lysine Production

<130> 1533.2640001

<150> 60/267,183

<151> 2001-02-08

<160> 25

<170> PatentIn version 3.1

<210> 1

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1266)

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gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct	96
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala	
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gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat	144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp	
35 40 45	

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt	192
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg	

50				55				60								
gaa Glu 65	atg Met	gat Asp	atg Met	ctc Leu	ctg Leu 70	act Thr	gct Ala	ggt Gly	gag Glu	cgt Arg 75	att Ile	tct Ser	aac Asn	gct Ala	ctc Leu 80	240
gtc Val	gcc Ala	atg Met	gct Ala	att Ile 85	gag Glu	tcc Ser	ctt Leu	ggc Gly	gca Ala 90	gaa Glu	gct Ala	caa Gln	tct Ser	ttc Phe 95	act Thr	288
ggc Gly	tct Ser	cag Gln	gct Ala 100	ggg Gly	gtg Val	ctc Leu	acc Thr	acc Thr 105	gag Glu	cgc Arg	cac His	gga Gly	aac Asn 110	gca Ala	cgc Arg	336
att Ile	gtt Val	gac Asp 115	gtc Val	aca Thr	ccg Pro	ggt Gly	cgt Arg 120	gtg Val	cgt Arg	gaa Glu	gca Ala	ctc Leu 125	gat Asp	gag Glu	ggc Gly	384
aag Lys	atc Ile 130	tgc Cys	att Ile	gtt Val	gct Ala	ggg Gly 135	ttt Phe	cag Gln	ggt Gly	gtt Val	aat Asn 140	aaa Lys	gaa Glu	acc Thr	cgc Arg	432
gat Asp 145	gtc Val	acc Thr	acg Thr	ttg Leu	ggg Gly 150	cgt Arg	ggg Gly	ggg Gly	tct Ser	gac Asp 155	acc Thr	act Thr	gca Ala	gtt Val	gcg Ala 160	480
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gac Asp	ggg Gly	gtg Val	tat Tyr 180	acc Thr	gct Ala	gac Asp	ccg Pro	cgc Arg 185	atc Ile	gtt Val	cct Pro	aat Asn 190	gca Ala	cag Gln	aag Lys	576
ctg Leu	gaa Glu	aag Lys 195	ctc Leu	agc Ser	ttc Phe	gaa Glu 200	gaa Glu	atg Met	ctg Leu	gaa Glu	ctt Leu	gct Ala 205	gct Ala	gtt Val	ggc Gly	624
tcc Ser	aag Lys 210	att Ile	ttg Leu	gtg Val	ctg Leu	cgc Arg 215	agt Ser	gtt Val	gaa Glu	tac Tyr	gct Ala 220	cgt Arg	gca Ala	ttc Phe	aat Asn	672
gtg Val 225	cca Pro	ctt Leu	cgc Arg	gta Val	cgc Arg 230	tcg Ser	tct Ser	tat Tyr	agt Ser	aat Asn 235	gat Asp	ccc Pro	ggc Gly	act Thr	ttg Leu 240	720
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ggg Gly	gtc Val	gca Ala	acc Thr 260	gac Asp	aag Lys	tcc Ser	gaa Glu	gcc Ala 265	aaa Lys	gta Val	acc Thr	gtt Val	ctg Leu 270	ggg Gly	att Ile	816
tcc Ser	gat Asp	aag Lys 275	cca Pro	ggc Gly	gag Glu	gct Ala	gcc Ala 280	aag Lys	gtt Val	ttc Phe	cgt Arg	gcg Ala 285	ttg Leu	gct Ala	gat Asp	864
gca Ala 290	gaa Glu	atc Ile	aac Asn	att Ile	gac Asp	atg Met 295	gtt Val	ctg Leu	cag Gln	aac Asn	gtc Val 300	tcc Ser	tct Ser	gtg Val	gaa Glu	912
gac Asp	ggc Gly	acc Thr	acc Thr	gac Asp	atc Ile	acg Thr	ttc Phe	acc Thr	tgc Cys	cct Pro	cgc Arg	gct Ala	gac Asp	gga Gly	cgc Arg	960

305	310	315	320	
cgt gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc				1008
Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr				
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aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct				1056
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala				
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ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg				1104
Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu				
	355	360	365	
cgc gat gtc aac gtg aac atc gaa ttg att tcc atc tct gag atc cgc				1152
Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg				
	370	375	380	
att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca				1200
Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala				
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ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat				1248
Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr				
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Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp				
35 40 45				
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg				
50 55 60				
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu				
65 70 75 80				
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr				

85

90

95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg  
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala

340

345

350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg  
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
405 410 415

Ala Gly Thr Gly Arg  
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<210> 3

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1035)

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atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt 96  
Met Arg Thr Phe Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg  
20 25 30

ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc 144  
Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
35 40 45

acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc 192  
Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
50 55 60

aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag 240  
Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
65 70 75 80

cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac 288

Gln	Tyr	Ala	Pro	Leu 85	Phe	Ala	Ala	Ala	Gly 90	Ala	Thr	Val	Val	Asp 95	Asn	
tct Ser	tct Ser	gct Ala	tgg Trp 100	cgc Arg	aag Lys	gac Asp	gac Asp	gag Glu 105	gtt Val	cca Pro	cta Leu	atc Ile	gtc Val 110	tct Ser	gag Glu	336
gtg Val	aac Asn	cct Pro 115	tcc Ser	gac Asp	aag Lys	gat Asp	tcc Ser 120	ctg Leu	gtc Val	aag Lys	ggc Gly	att Ile 125	att Ile	gcg Ala	aat Asn	384
cct Pro	aac Asn 130	tgc Cys	acc Thr	acc Thr	atg Met	gct Ala 135	gca Ala	atg Met	cca Pro	gtg Val	ctg Leu 140	aag Lys	cca Pro	ctg Leu	cac His	432
gat Asp 145	gcc Ala	gct Ala	ggg Gly	ctt Leu	gta Val 150	aag Lys	ctt Leu	cac His	gtt Val	tcc Ser 155	tct Ser	tac Tyr	cag Gln	gct Ala	gtt Val 160	480
tcc Ser	ggg Gly	tct Ser	ggg Gly	ctt Leu 165	gca Ala	ggg Gly	gtg Val	gaa Glu	acc Thr 170	ttg Leu	gca Ala	aag Lys	cag Gln	gtt Val 175	gct Ala	528
gca Ala	gtt Val	ggc Gly	gac Asp 180	cac His	aac Asn	gtt Val	gag Glu	ttc Phe 185	gtc Val	cat His	gat Asp	gga Gly	cag Gln 190	gct Ala	gct Ala	576
gac Asp	gca Ala	ggc Gly 195	gat Asp	gtc Val	gga Gly	cct Pro	tac Tyr 200	gtt Val	tcc Ser	cca Pro	atc Ile	gct Ala 205	tac Tyr	aac Asn	gtg Val	624
ctg Leu	cca Pro 210	ttc Phe	gcc Ala	gga Gly	aac Asn	ctc Leu 215	gtc Val	gat Asp	gac Asp	ggc Gly	acc Thr 220	ttc Phe	gaa Glu	acc Thr	gac Asp	672
gaa Glu 225	gag Glu	cag Gln	aag Lys	ctg Leu	cgc Arg 230	aac Asn	gaa Glu	tcc Ser	cgc Arg	aag Lys 235	att Ile	ctc Leu	ggc Gly	ctc Leu	cca Pro 240	720
gac Asp	ctc Leu	aag Lys	gtc Val	tca Ser 245	ggc Gly	acc Thr	tgc Cys	gtc Val	cgc Arg 250	gtg Val	ccg Pro	gtt Val	ttc Phe	acc Thr 255	ggc Gly	768
cac His	acg Thr	ctg Leu	acc Thr 260	att Ile	cac His	gcc Ala	gaa Glu	ttc Phe 265	gac Asp	aag Lys	gca Ala	atc Ile	acc Thr 270	gtc Val	gag Glu	816
cag Gln	gcg Ala	cag Gln 275	gag Glu	atc Ile	ttg Leu	ggg Gly	gcc Ala 280	gct Ala	tca Ser	ggc Gly	gtc Val	gag Glu 285	ctt Leu	gtc Val	gac Asp	864
gtc Val	cca Pro 290	acc Thr	cca Pro	ctt Leu	gca Ala	gct Ala 295	gcc Ala	ggc Gly	att Ile	gac Asp	gaa Glu 300	tcc Ser	ctc Leu	gtt Val	gga Gly	912
cgc Arg 305	atc Ile	cgt Arg	cag Gln	gac Asp	tcc Ser 310	act Thr	gtc Val	gac Asp	gac Asp	aac Asn 315	cgc Arg	ggg Gly	ctg Leu	gtt Val	ctc Leu 320	960
gtc Val	gta Val	tct Ser	ggc Gly	gat Asp 325	aac Asn	ctt Leu	cgc Arg	aag Lys	ggc Gly 330	gca Ala	gca Ala	ctg Leu	aac Asn 335	acc Thr	att Ile	1008

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1035

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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

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Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
50 55 60

Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
100 105 110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn  
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His  
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val  
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala  
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala  
180 185 190

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
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Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val  
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp  
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro  
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly  
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu  
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp  
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly  
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu  
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile  
325 330 335

Gln Ile Ala Glu Leu Leu Val Lys  
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<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(747)

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act att gtg gca gca gtc aat gag tcc gac gat ctg gag ctt gtt gca				96
Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala	20	25	30	
gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac aac ggc gct				144
Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala	35	40	45	
gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg ggc aac ctg				192
Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu	50	55	60	
gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga acc acg ggc				240
Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly	65	70	75	80
ttc gat aat gct cgt ttg gag cag gtt cgc gcc tgg ctt gaa gga aaa				288
Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys	85	90	95	
gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc tct gcg gtg				336
Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val	100	105	110	
ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc gaa tca gct				384
Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala	115	120	125	
gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca cct tca ggc				432
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly	130	135	140	
acc gcg atc cac act gct cag ggc att gct gcg gca cgc aaa gaa gca				480
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Arg Lys Glu Ala	145	150	155	160
ggc atg gac gca cag cca gat gcg acc gag cag gca ctt gag ggt tcc				528
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser	165	170	175	
cgt ggc gca agc gta gat gga atc cca gtt cac gca gtc cgc atg tcc				576
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser	180	185	190	
ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag ggt cag acc				624
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr	195	200	205	
ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt gca cca ggt				672
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly	210	215	220	
gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc cta gtc gta				720
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val	225	230	235	240
gga ctt gag cat tac cta ggc ctg taa				747
Gly Leu Glu His Tyr Leu Gly Leu	245			

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<212> PRT

<213> Corynebacterium glutamicum

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Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln  
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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala  
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Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala  
35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu  
50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly  
65 70 75 80

Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys  
85 90 95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val  
100 105 110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala  
115 120 125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly  
130 135 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala  
145 150 155 160

Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser  
165 170 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser  
180 185 190

Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr  
195 200 205

Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly  
210 215 220

Gly Leu Glu His Tyr Leu Gly Leu  
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<212> DNA

<213> Corynebacterium glutamicum

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gat tac aag aac atg acc aac atc cgc gta gct atc gta ggc tac gga 96  
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
20 25 30

aac ctg gga cgc agc gtc gaa aag ctt att gcc aag cag ccc gac atg 144  
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
35 40 45

gac ctt gta gga atc ttc tcg cgc cgg gcc acc ctc gac aca aag acg 192  
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
50 55 60

cca gtc ttt gat gtc gcc gac gtg gac aag cac gcc gac gac gtg gac 240  
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
65 70 75 80

gtg	ctg	ttc	ctg	tgc	atg	ggc	tcc	gcc	acc	gac	atc	cct	gag	cag	gca	288
Val	Leu	Phe	Leu	Cys	Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	
				85					90					95		

cca aag ttc gcg cag ttc gcc tgc acc gta gac acc tac gac aac cac 336  
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
100 105 110

cgc gac atc cca cgc cac cgc cag gtc atg aac gaa gcc gcc acc gca 384  
 Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
 115 120 125

gcc gcc aac gtt gca ctg gtc tct acc gcc tgg gat cca gga atg ttc 432

Ala	Gly	Asn	Val	Ala	Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	
130						135					140					
tcc	atc	aac	cgc	gtc	tac	gca	gcg	gca	gtc	tta	gcc	gag	cac	cag	cag	480
Ser	Ile	Asn	Arg	Val	Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	
145				150					155						160	
cac	acc	ttc	tgg	ggc	cca	ggt	ttg	tca	cag	ggc	cac	tcc	gat	gct	ttg	528
His	Thr	Phe	Trp	Gly	Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	
				165					170					175		
cga	cgc	atc	cct	ggc	ggt	caa	aag	gcc	gtc	cag	tac	acc	ctc	cca	tcc	576
Arg	Arg	Ile	Pro	Gly	Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	
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gaa	gaa	gcc	ctg	gaa	aag	gcc	cgc	cgt	ggc	gaa	gcc	ggc	gac	ctc	acc	624
Glu	Glu	Ala	Leu	Glu	Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	
		195				200						205				
gga	aag	caa	acc	cac	aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	gcg	gcc	672
Gly	Lys	Gln	Thr	His	Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	
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gac	cac	gag	cgc	atc	gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	720
Asp	His	Glu	Arg	Ile	Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	
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gtt	ggc	tac	gaa	gtc	gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttg	gac	768
Val	Gly	Tyr	Glu	Val	Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Leu	Asp	
			245						250					255		
gcc	gag	cac	acc	ggc	atg	cca	cac	ggc	gga	cac	gtg	atc	acc	acc	ggc	816
Ala	Glu	His	Thr	Gly	Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	
			260					265					270			
gac	acc	ggt	ggc	ttc	aac	cac	acc	gtg	gaa	tac	atc	ctg	aag	ctg	gac	864
Asp	Thr	Gly	Gly	Phe	Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	
		275					280					285				
cga	aac	cca	gat	ttc	acc	gct	tct	tca	cag	atc	gct	ttc	ggc	cgc	gca	912
Arg	Asn	Pro	Asp	Phe	Thr	Ala	Ser	Ser	Gln	Ile	Ala	Phe	Gly	Arg	Ala	
	290					295					300					
gct	cac	cgc	atg	aag	cag	cag	ggc	caa	agc	ggt	gct	ttc	acc	gtc	ctc	960
Ala	His	Arg	Met	Lys	Gln	Gln	Gly	Gln	Ser	Gly	Ala	Phe	Thr	Val	Leu	
	305				310					315					320	
gaa	gtt	gct	cca	tac	ttg	ctc	tcc	ccg	gag	aac	ttg	gat	gat	ctg	atc	1008
Glu	Val	Ala	Pro	Tyr	Leu	Leu	Ser	Pro	Glu	Asn	Leu	Asp	Asp	Leu	Ile	
				325					330					335		
gca	cgc	gac	gtc	taa												1023
Ala	Arg	Asp	Val													
			340													

<210> 8

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

Met	His	Phe	Gly	Lys	Leu	Asp	Gln	Asp	Ser	Ala	Thr	Thr	Ile	Leu	Glu	1	5	10	15
Asp	Tyr	Lys	Asn	Met	Thr	Asn	Ile	Arg	Val	Ala	Ile	Val	Gly	Tyr	Gly	20	25	30	
Asn	Leu	Gly	Arg	Ser	Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	35	40	45	
Asp	Leu	Val	Gly	Ile	Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	50	55	60	
Pro	Val	Phe	Asp	Val	Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	65	70	75	80
Val	Leu	Phe	Leu	Cys	Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	85	90	95	
Pro	Lys	Phe	Ala	Gln	Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	100	105	110	
Arg	Asp	Ile	Pro	Arg	His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	115	120	125	
Ala	Gly	Asn	Val	Ala	Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	130	135	140	
Ser	Ile	Asn	Arg	Val	Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	145	150	155	160
His	Thr	Phe	Trp	Gly	Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	165	170	175	
Arg	Arg	Ile	Pro	Gly	Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	180	185	190	
Glu	Glu	Ala	Leu	Glu	Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	195	200	205	
Gly	Lys	Gln	Thr	His	Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	210	215	220	
Asp	His	Glu	Arg	Ile	Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	225	230	235	240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp  
245 250 255

Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly  
260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp  
275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala  
290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu  
305 310 315 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile  
325 330 335

Ala Arg Asp Val  
340

<210> 9

<211> 753

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(753)

<400> 9

gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct 48  
Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
1 5 10 15

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg 96  
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat 144  
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc 192  
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

tat	atc	cga	ggc	att	tct	cgg	tcc	gcg	acc	cat	gaa	ttg	gtc	cga	cac	288
Tyr	Ile	Arg	Gly	Ile	Ser	Arg	Ser	Ala	Thr	His	Glu	Leu	Val	Arg	His	
			85					90						95		

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga 336  
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

gaa tcg gaa gta gtg gtg ccc act ctc atc gat gaa gat ccg cag ttg 384  
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
115 120 125

cgt gaa ctt ttc atg cac gcc atg gat gag tct cgg ttc gct ttc aat 432  
 Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
 130 135 140

gag ctg ctt aat gcg ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca 480  
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
145 150 155 160

ctt tta agg aaa aag cag gct cgt caa gca gct cgc gct gtg ctg ccc 528  
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
165 170 175

aac gct aca gag tcc aga atc gtg gtg tct gga aac ttc cgc acc tgg 576  
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
180 185 190

agg cat ttc att ggc atg cga gcc agt gaa cat gca gac gtc gaa atc 624  
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
195 200 205

cgc gaa gta gcg gta gga tgt tta aga aag ctg cag gta gca gcg cca 672  
 Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
 210 215 220

act gtt ttc ggt gat ttt gag att gaa act ttg gca gac gga tcg caa 720  
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
225 230 235 240

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atg gca aca agc ccg tat gtc atg gac ttt taa      753
Met Ala Thr Ser Pro Tyr Val Met Asp Phe
                245                250

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<210> 10

<211> 250

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 10

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
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Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
195 200 205

Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe  
245 250

<210> 11

<211> 1338



<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1338)

<400> 11

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro	
1 5 10 15	

cgc aat gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg	96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val	
20 25 30	

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc	144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val	
35 40 45	

gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc	192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe	
50 55 60	

ggt gga cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag	240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys	
65 70 75 80	

acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca	288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala	
85 90 95	

tcc atc aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc	336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser	
100 105 110	

cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg	384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala	
115 120 125	

ttg gtt caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa	432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu	
130 135 140	

cta gaa ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac	480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp	
145 150 155 160	

gtg ttg atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc	528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe	
165 170 175	

atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc	576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser	
180 185 190	

atg gct aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca  
 Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro  
 1 5 10 15  
 cgc aat gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg  
 Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val  
 20 25 30  
 cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc  
 Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val  
 35 40 45  
 gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc  
 Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe  
 50 55 60  
 ggt gga cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag  
 Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys  
 65 70 75 80  
 acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca  
 Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala  
 85 90 95  
 tcc atc aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc  
 Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser  
 100 105 110  
 cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg  
 Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala  
 115 120 125  
 ttg gtt caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa  
 Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu  
 130 135 140  
 cta gaa ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac  
 Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp  
 145 150 155 160  
 gtg ttg atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc  
 Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe  
 165 170 175  
 atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc  
 Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser  
 180 185 190

ggt Gly	tcc Ser	gca Ala 195	ttc Phe	gaa Glu	gca Ala	gca Ala	aaa Lys 200	gcc Ala	gcc Ala	aac Asn	aac Asn	gca Ala 205	gaa Glu	aac Asn	ctg Leu	624
aac Asn	ctg Leu 210	gtt Val	ggc Gly	ctg Leu	cac His	tgc Cys 215	cac His	gtt Val	ggt Gly	tcc Ser	cag Gln 220	gtg Val	ttc Phe	gac Asp	gcc Ala	672
gaa Glu 225	ggc Gly	ttc Phe	aag Lys	ctg Leu	gca Ala 230	gca Ala	gaa Glu	cgc Arg	gtg Val 235	ttg Leu	ggc Gly	ctg Leu	tac Tyr	tca Ser	cag Gln 240	720
atc Ile	cac His	agc Ser	gaa Glu	ctg Leu 245	ggc Gly	gtt Val	gcc Ala	ctt Leu	cct Pro 250	gaa Glu	ctg Leu	gat Asp	ctc Leu	ggt Gly 255	ggc Gly	768
gga Gly	tac Tyr	ggc Gly	att Ile 260	gcc Ala	tat Tyr	acc Thr	gca Ala	gct Ala 265	gaa Glu	gaa Glu	cca Pro	ctc Leu 270	aac Asn	gtc Val	gca Ala	816
gaa Glu	gtt Val	gcc Ala 275	tcc Ser	gac Asp	ctg Leu	ctc Leu	acc Thr 280	gca Ala	gtc Val	gga Gly	aaa Lys 285	atg Met	gca Ala	gcg Ala	gaa Glu	864
cta Leu	ggc Gly 290	atc Ile	gac Asp	gca Ala	cca Pro	acc Thr 295	gtg Val	ctt Leu	gtt Val	gag Glu	ccc Pro 300	ggc Gly	cgc Arg	gct Ala	atc Ile	912
gca Ala 305	ggc Gly	ccc Pro	tcc Ser	acc Thr	gtg Val 310	acc Thr	atc Ile	tac Tyr	gaa Glu	gtc Val 315	ggc Gly	acc Thr	acc Thr	aaa Lys	gac Asp 320	960
gtc Val	cac His	gta Val	gac Asp	gac Asp 325	gac Asp	aaa Lys	acc Thr	cgc Arg	cgt Arg 330	tac Tyr	atc Ile	gcc Ala	gtg Val	gac Asp 335	gga Gly	1008
ggc Gly	atg Met	tcc Ser	gac Asp 340	aac Asn	atc Ile	cgc Arg	cca Pro	gca Ala 345	ctc Leu	tac Tyr	ggc Gly	tcc Ser 350	gaa Glu	tac Tyr	gac Asp	1056
gcc Ala	cgc Arg	gta Val 355	gta Val	tcc Ser	cgc Arg	ttc Phe	gcc Ala 360	gaa Glu	gga Gly	gac Asp	cca Pro	gta Val 365	agc Ser	acc Thr	cgc Arg	1104
atc Ile	gtg Val 370	ggc Gly	tcc Ser	cac His	tgc Cys	gaa Glu 375	tcc Ser	ggc Gly	gat Asp	atc Ile	ctg Leu 380	atc Ile	aac Asn	gat Asp	gaa Glu	1152
atc Ile 385	tac Tyr	cca Pro	tct Ser	gac Asp	atc Ile 390	acc Thr	agc Ser	ggc Gly	gac Asp	ttc Phe 395	ctt Leu	gca Ala	ctc Leu	gca Ala	gcc Ala 400	1200
acc Thr	ggc Gly	gca Ala	tac Tyr	tgc Cys 405	tac Tyr	gcc Ala	atg Met	agc Ser	tcc Ser 410	cgc Arg	tac Tyr	aac Asn	gcc Ala	ttc Phe 415	aca Thr	1248
cgg Arg	ccc Pro	gcc Ala	gtc Val 420	gtg Val	tcc Ser	gtc Val	cgc Arg	gct Ala 425	ggc Gly	agc Ser	tcc Ser	cgc Arg	ctc Leu 430	atg Met	ctg Leu	1296
cgc Arg	cgc Arg	gaa Glu 435	acg Thr	ctc Leu	gac Asp	gac Asp	atc Ile 440	ctc Leu	tca Ser	cta Leu	gag Glu 445	gca Ala	taa			1338

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<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro  
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Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val  
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val  
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe  
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys  
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala  
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser  
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala  
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu  
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp  
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe  
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser  
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu  
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala  
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln  
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly  
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala  
260 265 270

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu  
275 280 285

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile  
290 295 300

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp  
305 310 315 320

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly  
325 330 335

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp  
340 345 350

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg  
355 360 365

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu  
370 375 380

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala  
385 390 395 400

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr  
405 410 415

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu  
420 425 430

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala  
435 440 445

<210> 13

<211> 365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser	
1 5 10 15	

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg	96
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala	
20 25 30	

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat	144
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp	
35 40 45	

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc	192
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile	
50 55 60	

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg	240
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met	
65 70 75 80	

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac	288
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His	
85 90 95	

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga	336
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly	
100 105 110	

gaa tcg gaa gta gtg gtg ccc act ctc at	365
Glu Ser Glu Val Val Val Pro Thr Leu Ile	
115 120	

<210> 14

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser

1	5	10	15
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala	20	25	30
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp	35	40	45
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile	50	55	60
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met	65	70	75
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His	85	90	95
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly	100	105	110
Glu Ser Glu Val Val Val Pro Thr Leu Ile	115	120	

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 <211> 551  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 gccaccggag ttaccgaaga tgggtgccgtg cttttgcct tgggcaggga ccttgacaaa 180  
 gccacgctg atatcgccaa gtgagggatc agaatagtgc atgggcacgt cgatgctgcc 240  
 acattgagcg gaggcaatat ctacctgagg tgggcattct tcccagcgga tgttttcttg 300  
 cgtgctgca gtgggcattg ataccaaaaa ggggctaagc gcagtcgagg cggcaagaac 360  
 tgctactacc ttttttattg tcgaacgggg cattacggct ccaaggacgt ttgttttctg 420  
 ggtcagttac cccaaaaagc atatacagag accaatgatt tttcattaaa aaggcaggga 480  
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 catgacacca g 551

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 <213> Artificial Sequence

<220>  
 <223> Consensus Sequence of Protein Sequence Alignment

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 <221> MISC\_FEATURE  
 <222> (40)..(40)  
 <223> May be either Cys or Val

<220>  
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 <222> (317)..(317)  
 <223> May be either Ser or Ala

<220>  
 <221> MISC\_FEATURE  
 <222> (345)..(345)  
 <223> May be either Gly or Asp

<220>  
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 <222> (380)..(380)  
 <223> May be either Thr or Ile

<400> 16

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
 1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30

Gly Asn Asp Val Val Val Val Xaa Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
260 265 270

1  
2  
3  
4  
5  
6  
7  
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Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
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Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
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Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Xaa Asp Gly Arg  
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Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
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Asn Val Leu Tyr Asp Asp Gln Val Xaa Lys Val Ser Leu Val Gly Ala  
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Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
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Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Xaa Ser Glu Ile Arg  
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Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
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